Amendments to the Specification:

Please amend the paragraph beginning on page 54, line 27 as follows:

-- To test for the presence of *sgfp*(S65T) in genomic DNA of putatively transformed lines, 500 ng of genomic DNA was amplified by PCR using either of two primer sets, Act1int1 (5'-TCGTCAGGCT TAGATGTG-3') (SEQ ID NO: 1) plus sGFP4R (5'-agaggtaccTTACTTGTACAGCTCGTC-3') (SEQ ID NO: 2) for pAct1IsGFP-1 transformants and sGFP3 (5'-ccctctagaCCATGGTGAGCAAGGGCGAG-3') (SEQ ID NO: 3) plus sGFP4R for pDhsGFP1 transformants. The presence of *bar* was tested using the primer set, BAR5F (5'-CATCGAGACAAGCACGGTCAACTTC-3') (SEQ ID NO: 4) plus BAR1R (5'-ATATCCGAGCGCCTCGTGCATGCG-3') (SEQ ID NO: 5) (Lemaux *et al.*, 1996). Amplifications were performed in a 25 µl reaction with *Taq* DNA polymerase according to a protocol described by Cho *et al*, (1998). For DNA hybridization analysis, 10 µg of total genomic DNA from leaf tissue of each line was digested with *Sac*I, separated on a 1.0% agarose gel, transferred to Zeta-Probe GT membrane and hybridized with a radiolabeled *sgfp*(S65T)- specific probe following the manufacturer's instructions. Digestion with *Sac*I yielded a 1.54-kb fragment containing 0.47-kb actin1 intron, 0.72-kb *sgfp*(S65T) and 0.35-kb *nos* from pAct1IsGFP-1 (Figure 1A). The *sgfp*(S65T)-containing 0.72-kb *Nco*I- *Not*I fragment from pAct1IsGFP-1 was purified using a QIAEX gel extraction kit and labeled with α-^{32}P-dCTP using random primers. --

Please amend the paragraph beginning on page 70, line 27 as follows:

-- To test for the presence of *uidA*, *bar*, *sgfp*(S65T) and *hpt*, genomic DNA was isolated from leaf tissues of putative, independently transformed lines, derived from different pieces of bombarded tissue that were tracked during selection. Five hundred ng DNA was used in PCR amplifications using the primer sets for *uidA*, UIDA1 (5'-agcggccgcaTTACGTCCTGTAGAAACC-3') (SEQ ID NO: 6) plus UID2R (5'-agagctcTCATTGTTTGCCTCCCTG-3') (SEQ ID NO: 7) (Cho *et al.*, 1998); for *bar*, BAR5F (5'-CATCGAGACAAGCACGGTCAACTTC-3') (SEQ ID NO: 4) plus BAR1R (5'-

ATATCCGAGCGCCTCGTGCATGCG-3') (SEQ ID NO: 5) (Lemaux *et al.*, 1996; Cho *et al.*, 1998); for *sgfp*(S65T), Act1int1 (5'- TCGTCAGGCT TAGATGTG-3') (SEQ ID NO: 1) plus sGFP4R (5'- agaggtaccTTACTTGTACAGCTCGTC-3') (SEQ ID NO: 2); and for *hpt*, HPT6F (5'-AAGCCTGAACTCACCGCGACG-3') (SEQ ID NO: 8) plus HPT5R (5'-AAGACCAATGCGGAGCATATAC-3') (SEQ ID NO: 9) (Cho *et al.*, 1998). Amplifications were performed in a 25 µl reaction with *Taq* DNA polymerase (Promega, Madison, WI) as described (Cho *et al.*, 1998). --

Please amend the paragraph beginning on page 78, line 28 as follows:

-- Total genomic DNA from leaf tissues of putatively transformed plants was purified as described (Dellaporta, 1993). To test for the presence of *uidA* and *hpt* in genomic DNA of putatively transformed lines, 500 ng of genomic DNA was amplified by PCR using the primer set, UIDA1 (5'- agcggccgcaTTACGTCCTGTAGAAACC-3') (SEQ ID NO: 6) plus UID2R (5'-agagctcTCATTGTTTGCCTCCCTG-3') (SEQ ID NO: 7) (Lemaux *et al.*, 1996) or HPT6F (5'-AAGCCTGAACTCACCGCGACG-3') (SEQ ID NO: 8) plus HPT5R (5'-AAGACCAATGCGGAGCATATAC-3') (SEQ ID NO: 9) (Cho *et al.*, 1998b), respectively. Amplifications were performed in a 25-µl reaction with *Taq* DNA polymerase (Promega, Madison, WI) according to a protocol described by Cho *et al.*, (Cho *et al*, 1998b). For DNA hybridization analysis, 10 µg of total genomic DNA from leaf tissue of each line was digested with *Bam*HI and *Eco*RI, separated on a 1.0% agarose gel, transferred to Zeta-Probe GT membrane (Bio-Rad, Hercules, CA) and hybridized with a radiolabeled *uidA*-specific probe following manufacturer's instructions. The *uidA*-containing 1.9-kb *Bam*HI-*Sac*I fragment from pAHC15 was isolated with QIAEX gel extraction kit (QIAGEN, Chatsworth, CA) and labeled with α-^{32}P-dCTP using random priming according to manufacturer's instructions (Promega, Madison, WI). --

Please amend the paragraph beginning on page 103, line 15 as follows:

-- To test for the presence of *uidA*, *bar* and *hpt* in genomic DNA of putative, independently transformed lines, 500 ng of genomic DNA, isolated from leaf tissues, was amplified by PCR using the primer sets, UIDA1 (5'- agcggccgcaTTACGTCCTGTAGAAACC-3') (SEQ ID NO: 6) plus UID2R (5'- agagctcTCATTGTTTGCCTCCCTG-3') (SEQ ID NO: 7) (Cho *et al.*, 1998b), BAR5F (5'- CATCGAGACAAGCACGGTCAACTTC-3') (SEQ ID NO: 4) plus BAR1R (5'- ATATCCGAGCGCCTCGTGCATGCG-3') (SEQ ID NO: 5) (Lemaux *et al.*, 1996), and HPT6F (5'- AAGCCTGAACTCACCGCGACG-3') (SEQ ID NO: 8) plus HPT5R (5'- AAGACCAATGCGGAGCATATAC-3') (SEQ ID NO: 9) (Cho *et al.*, 1998b), respectively. Amplifications were performed in 25-µl reaction with *Taq* DNA polymerase (Promega, Madison, WI) as described (Cho *et al.*, 1998). --

Please amend the paragraph beginning on page 111, line 19 as follows:

-- *Genomic DNA isolation, polymerase chain reaction (PCR) and DNA blot hybridization analysis.* To determine the presence of *hpt, sgfp*(S65T), and *uidA* genes in genomic DNA of putative, independently transformed lines, 500 ng of genomic DNA isolated from leaf tissues (Dellapora, 1991) was used in 25-µl PCR reactions with *Taq* DNA polymerase (Promega, Madison, WI) as previously described (Cho *et al.*, 1998b). The individual 2 to 5 plants per line were tested for PCR reactions. The primers sets for *hpt* were HPT6F (5'- AAGCCTGAACTCACCGCGACG-3') (SEQ ID NO: 8) and HPT5R (5'- AAGACCAATGCGGAGCATATAC-3') (SEQ ID NO: 9) (Cho *et al.*, 1998b); for *sgfp*(S65T), Act1int1 (5'- TCGTCAGGCT TAGATGTG-3') (SEQ ID NO: 1) and sGFP4R (5'- agaggtaccTTACTTGTACAGCTCGTC-3') (SEQ ID NO: 2) (Cho *et al.*, 2000); for *uidA*, UIDA1 (5'- agcggccgcaTTACGTCCTGTAGAAACC-3') (SEQ ID NO: 6) and UID2R (5'- agagctcTCATTGTTTGCCTCCCTG-3') (SEQ ID NO: 7) (Cho *et al.*, 1998b). --